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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/865,321

DATE: 09/05/2001

TIME: 19:13:28

Input Set : A:\Peach571.app

Output Set: N:\CRF3\09052001\I865321.raw

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3 <110> APPLICANT: Peach, Robert J.
4     Naemura, Joseph R
5     Linsley, Peter S.
6     Bajorath, Jürgen
8 <120> TITLE OF INVENTION: SOLUBLE CTLA4 MUTANT MOLECULES AND USES THEREOF
10 <130> FILE REFERENCE: DB28NP/30436.57USU1
12 <140> CURRENT APPLICATION NUMBER: 09/865,321
13 <141> CURRENT FILING DATE: 2001-05-23
15 <150> PRIOR APPLICATION NUMBER: 60/287,576
16 <151> PRIOR FILING DATE: 2000-05-26
18 <150> PRIOR APPLICATION NUMBER: 60/214,065
19 <151> PRIOR FILING DATE: 2000-06-26
21 <160> NUMBER OF SEQ ID NOS: 8
23 <170> SOFTWARE: PatentIn Ver. 2.1
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26 <211> LENGTH: 41
27 <212> TYPE: DNA
28 <213> ORGANISM: Artificial Sequence
30 <220> FEATURE:
31 <223> OTHER INFORMATION: Description of Artificial Sequence:Oncostatin M
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56 <220> FEATURE:
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62 ggcatcgcta gctttgtgtg tgagtatgca tctccaggca aatatactga ggtccgggtg 180
63 acagtgcctc ggcaggctga cagccagggtg actgaagtct gtgcggcaac ctacatgatg 240
64 gggaatgagt tgaccttctt agatgattcc atctgcacgg gcacctccag tggaaatcaa 300
65 gtgaacctca ctatccaagg actgagggcc atggacacgg gactctacat ctgcaagggtg 360
66 gagctcatgt acccaccgcc atactacgag ggcataggca acggaaccca gatttatgta 420
67 attgatccag aaccgtgccc agattctgat caggagccca aatcttctga caaaactcac 480

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68 acatccccac cgtccccagc acctgaactc ctgggggggat cgtcagtctt cctcttcccc 540
69 ccaaaaccca aggacaccct catgatctcc cggacccctg aggtcacatg cgtgggtggtg 600
70 gacgtgagcc acgaagaccc tgaggtcaag ttcaactggt acgtggacgg cgtggaggtg 660
71 cataatgcca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg tgtggtcagc 720
72 gtcttcaccg tcctgcacca ggactggctg aatggcaagg agtacaagtg caaggtctcc 780
73 aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga 840
74 gaaccacagg tgtacaccct gcccccatcc cgggatgagc tgaccaagaa ccaggtcagc 900
75 ctgacctgcc tggtaaagg cttctatccc agcgacatcg ccgtggagtg ggagagcaat 960
76 gggcagccgg agaacaacta caagaccacg cctcccgctc tggactccga cggctccttc 1020
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94 Leu Leu Phe Pro Ser Met Ala Ser Met Ala Met His Val Ala Gln Pro
95 20 25 30
97 Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu
98 35 40 45
100 Tyr Ala Ser Pro Gly Lys Tyr Thr Glu Val Arg Val Thr Val Leu Arg
101 50 55 60
103 Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met
104 65 70 75 80
106 Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser
107 85 90 95
109 Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp
110 100 105 110
112 Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr
113 115 120 125
115 Tyr Glu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu
116 130 135 140
118 Pro Cys Pro Asp Ser Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His
119 145 150 155 160
121 Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Gly Gly Ser Ser Val
122 165 170 175
124 Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
125 180 185 190
127 Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
128 195 200 205
130 Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
131 210 215 220
133 Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
134 225 230 235 240

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136 Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
137          245          250          255
139 Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
140          260          265          270
142 Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
143          275          280          285
145 Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
146          290          295          300
148 Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
149 305          310          315          320
151 Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
152          325          330          335
154 Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
155          340          345          350
157 Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
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165 <211> LENGTH: 1152
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175 ggcacgcgta gctttgtgtg tgagtatgca tctccaggca aagccactga ggtccgggtg 180
176 acagtgcctc ggcaggctga cagccagggt actgaagtct gtgcggcaac ctacatgatg 240
177 gggaatgagt tgaccttctt agatgattcc atctgcacgg gcacctccag tggaaatcaa 300
178 gtgaacctca ctatccaagg actgagggcc atggacacgg gactctacat ctgcaagggtg 360
179 gagctcatgt acccaccgcc atactacgag ggcataggca acggaaccca gatttatgta 420
180 attgatccag aaccgtgccc agattctgat caggagccca aatcttctga caaaactcac 480
181 acatccccac cgtccccagc acctgaactc ctggggggat cgtcagtctt cctcttcccc 540
182 ccaaaaccca aggacaccct catgatctcc cggaccctg aggtcacatg cgtggtggtg 600
183 gacgtgagcc acgaagaccc tgaggtcaag ttcaactggt acgtggacgg cgtggagggtg 660
184 cataatgcc aagacaaagc gcgggaggag cagtacaaca gcacgtaccg tgtggtcagc 720
185 gtcctcaccg tcctgcacca ggactggctg aatggcaagg agtacaagtg caaggtctcc 780
186 aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga 840
187 gaaccacagg tgtacacctt gcccccatcc cgggatgagc tgaccaagaa ccaggtcagc 900
188 ctgacctgcc tggtaaagg cttctatccc agcgacatcg ccgtggagtg ggagagcaat 960
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195 <210> SEQ ID NO: 6
196 <211> LENGTH: 383
197 <212> TYPE: PRT
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200 &lt;220&gt; FEATURE:

201 &lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence:L104EIg

203 &lt;400&gt; SEQUENCE: 6

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208           20           25           30
210 Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu
211           35           40           45
213 Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg
214           50           55           60
216 Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met
217           65           70           75           80
219 Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser
220           85           90           95
222 Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp
223           100          105          110
225 Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr
226           115          120          125
228 Tyr Glu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu
229           130          135          140
231 Pro Cys Pro Asp Ser Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His
232           145          150          155          160
234 Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly Gly Ser Ser Val
235           165          170          175
237 Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
238           180          185          190
240 Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
241           195          200          205
243 Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
244           210          215          220
246 Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
247           225          230          235          240
249 Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
250           245          250          255
252 Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
253           260          265          270
255 Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
256           275          280          285
258 Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
259           290          295          300
261 Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
262           305          310          315          320
264 Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
265           325          330          335
267 Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
268           340          345          350
270 Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
271           355          360          365

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283 <223> OTHER INFORMATION: Description of Artificial Sequence:CTLA4Ig ✓
285 <400> SEQUENCE: 7
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288 ggcacgctga gctttgtgtg tgagtatgca tctccaggca aagccactga ggtccgggtg 180
289 acagtgcctc ggcaggctga cagccagggt actgaagtct gtgcggcaac ctacatgatg 240
290 gggaatgagt tgaccttcct agatgattcc atctgcacgg gcacctccag tggaaatcaa 300
291 gtgaacctca ctatccaagg actgagggcc atggacacgg gactctacat ctgcaagggtg 360
292 gagctcatgt acccaccgcc atactacctg ggcataggca acggaaccca gatttatgta 420
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294 acatccccac cgtccccagc acctgaactc ctgggtggat cgtcagctct cctcttcccc 540
295 ccaaaaccca aggacaccct catgatctcc cggacccttg aggtcacatg cgtgggtgggtg 600
296 gacgtgagcc acgaagaccc tgaggtcaag ttcaactggg acgtggacgg cgtggaggtg 660
297 cataatgcc aagacaaagcc gcgggaggag cagtacaaca gcacgtaccg ggtggtcagc 720
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321      20                      25                      30
323 Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu
324      35                      40                      45
326 Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg
327      50                      55                      60
329 Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met
330      65                      70                      75                      80
332 Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser
333      85                      90                      95
335 Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp

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**VERIFICATION SUMMARY**

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